

SEQUENCE LISTING

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<120> Gamma-Conopeptides

<130> 2314-147-sq2

<140>

<141>

<150> US 60/069,706

<151> 1997-12-16

<160> 47

<170> PatentIn Ver. 2.0

<210> 1

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic formula
of gamma-conopeptides

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1, 2, 3, 4, 5, and 6 may be
des-Xaa or any amino acid; Xaa at residues 8, 9,
10, 11 and 12 may be any amino acid; Xaa at
residue 13 may be des-Xaa or any amino acid.

<220>

<221> PEPTIDE

<222> (15)..(19)

<223> Xaa at residues 15, 16, 17 and 18 may be any amino
acid; Xaa at residue 19 is Glu,
gamma-carboxyglutamate or Gln.

<220>

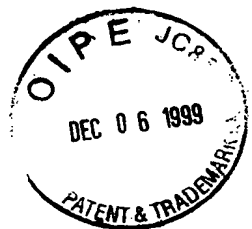
<221> PEPTIDE

<222> (22)..(28)

<223> Xaa at residues 22, 23 and 24 may be any amino
acid; Xaa at residue 25 may be des-Xaa or any
amino acid; Xaa at residues 27, 28 and 29 may be
any amino acid.

<220>

<221> PEPTIDE



af

1,0320

<222> (30)..(42)

<223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40

<210> 2

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic sequence of gamma-conopeptides.

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1, 2, 3, 4, 5 and 6 may be des-Xaa or any amino acid; Xaa at residues 8, 9, 10, 11 and 12 may be any amino acid; Xaa at residue 13 may be des-Xaa or any amino acid.

<220>

<221> PEPTIDE

<222> (15)..(22)

<223> Xaa at residues 15, 16, 17 and 18 may be any amino acid; Xaa at residue 19 is Glu, gamma-carboxyglutamate or Gln; Xaa at residue 22 is Ser or Thr.

<220>

<221> PEPTIDE

<222> (23)..(29)

<223> Xaa at residues 23 and 24 may be any amino acid; Xaa at residue 25 may be des-Xaa or any amino acid; Xaa at residues 27, 28 and 29 may be any amino acid.

<220>

<221> PEPTIDE

<222> (30)..(42)

<223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 2

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40

<210> 3
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic formula
 of gamma-conopeptides

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 1 is any amino acid; Xaa at
 residues 2, 3, 4, 5 and 6 may be des-Xaa or any
 amino acid; Xaa at residues 8, 9, 10, 11, 12 and
 13 may be any amino acid.

<220>
 <221> PEPTIDE
 <222> (27)..(39)
 <223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36
 and 37 may be any amino acid; Xaa at residues 38
 and 39 may be des-Xaa or any amino acid.

<220>
 <221> PEPTIDE
 <222> (15)..(19)
 <223> Xaa at residues 15, 16, 17 and 18 may be any amino
 acid; Xaa at residue 19 is Glu or
 gamma-carboxyglutamate.

<400> 3
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35

<210> 4
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic
 sequence of gamma-conopeptides.

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 1 is any amino acid; Xaa at
 residues 2, 3, 4, 5 and 6 may be des-Xaa or any
 amino acid; Xaa at residues 8, 9, 10, 11, 12 and
 13 may be any amino acid.

<220>

<221> PEPTIDE
 <222> (15)..(19)
 <223> Xaa at residue 15 is Ser or Thr; Xaa at residues
 16, 17 and 18 may be any amino acid; Xaa at
 residue 19 is Glu or gamma-carboxyglutamate.

<220>
 <221> PEPTIDE
 <222> (27)..(39)
 <223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36
 and 37 may be any amino acid; Xaa at residues 38
 and 39 may be des-Xaa or any amino acid.

<400> 4
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35

<210> 5
 <211> 34
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic
 sequence of gamma-conopeptides.

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residues 1 and 2 may be des-Xaa or any
 amino acid; Xaa at residue 3 is Asp, Glu or
 gamma-carboxyglutamate; Xaa at residues 5 and 6
 may be any amino acid.

<220>
 <221> PEPTIDE
 <222> (7)..(16)
 <223> Xaa at residue 7 is Trp or 6-bromo-Trp; Xaa at
 residues 9, 10, 13 and 14 may be any amino acid;
 Xaa at residue 16 is Glu or
 gamma-carboxyglutamate.

<220>
 <221> PEPTIDE
 <222> (28)..(34)
 <223> Xaa at residues 28, 30, 31, 32, 33 and 34 may be
 any amino acid.

<400> 5
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Cys Thr Xaa Xaa Ser Xaa
 1 5 10 15

Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Xaa Xaa Xaa
 20 25 30

Xaa Xaa

<210> 6
 <211> 32
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residues 14 and 26 are Glu or gamma-carboxyglutamate; Xaa at residue 31 is Pro or hydroxy-Pro.

<400> 6
 Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
 1 5 10 15
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
 20 25 30

<210> 7
 <211> 34
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa at residues 1, 7 and 34 are Trp or 6-bromo-Trp; Xaa at residues 3 and 16 are Glu or gamma-carboxyglutamate; Xaa at residues 31 and 32 are Pro or hydroxy-Pro.

<400> 7
 Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa
 1 5 10 15
 Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa
 20 25 30

Asp Xaa

<210> 8
 <211> 39
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(39)
 <223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or 6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or gamma-carboxyglutamate; Xaa at residues 34, 36 and 37 are Pro or hydroxy-Pro.

<400> 8
 Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg

1 5 10 15
 Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Xaa Leu
 20 25 30

Met Xaa Phe Xaa Xaa Asp Xaa
 35

<210> 9
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 9, 13 and 17 are Glu or
 gamma-carboxyglutamate.

<400> 9
 Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr
 1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe
 20 25

<210> 10
 <211> 34
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa at residues 2, 3, 10 and 32 are Trp or
 6-bromo-Trp; Xaa at residues 18, 26 and 33 are Glu
 or gamma-carboxyglutamate; Xaa at residue 12 is
 Pro or hydroxy-Pro.

<400> 10
 Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn
 1 5 10 15

Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa Thr Cys Ile Phe Gly Xaa
 20 25 30

Xaa Val

<210> 11
 <211> 31
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;
 Xaa at residues 5, 18, 22 and 25 are Glu or
 gamma-carboxyglutamate; Xaa at residue 16 is Pro
 or hydroxy-Pro.

<400> 11
Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa
1 5 10 15

Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa
20 25 30

<210> 12
<211> 32
<212> PRT
<213> Conus gloriamaris

<220>
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at
residue 1 is Glu or gamma-carboxyglutamate; Xaa at
residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12
Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys
1 5 10 15
Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu
20 25 30

<210> 13
<211> 29
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;
Xaa at residues 5, 16 and 23 are Glu or
gamma-carboxyglutamate; Xaa at residue 10 is Pro
or hydroxy-Pro.

<400> 13
Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa
1 5 10 15

Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile
20 25

<210> 14
<211> 27
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at
residues 9, 12, 13 and 17 are Glu or
gamma-carboxyglutamate.

<400> 14
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser
1 5 10 15

Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe
20 25

<210> 15
<211> 26
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;
Xaa at residue 16 is Glu or
gamma-carboxyglutamate.

<400> 15
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa
1 5 10 15

Cys Cys Ser Met Ser Cys Asp Met Tyr Cys
20 25

<210> 16
<211> 323
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (1)..(153)

<400> 16
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu
1 5 10 15

cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tgc 96
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser
20 25 30

gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro
35 40 45

ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggctttt 193
Pro Asp Trp
50

gttctctttt gaagaatttt aacgagtga caaaaaagtg gactagcatg tttccttttc 253

cctttgcaaa atcaatgatg gaggtaaaag cctcccattt tgtcttcatc aataaagaac 313

ttatcatcat 323

<210> 17
<211> 51
<212> PRT

<213> Conus textile

<400> 17

Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu
1 5 10 15

Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser
20 25 30

Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro
35 40 45

Pro Asp Trp
50

<210> 18

<211> 510

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (95)..(337)

<400> 18

tgactcgcca tctctctctt cagtctccct gacagctgcc ttcagtcgac cctgccgtca 60

tctcaacgca cacttgaagt gaaaaacctt tctc atg gag aaa ctg aca att ctg 115
Met Glu Lys Leu Thr Ile Leu
1 5

ctt ctt gtt gct gct gta ctg ttg tct atc cag gcc cta aat caa gaa 163
Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu
10 15 20

aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211
Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro
25 30 35

gct gag cgt tgg tgg cgg tgg gga gga tgc atg gct tgg ttt ggg ctt 259
Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu
40 45 50 55

tgt tct agg gac tct gaa tgt tgt tct aat agt tgt gac gta acg cgc 307
Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg
60 65 70

tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357
Cys Glu Leu Met Pro Phe Pro Pro Asp Trp
75 80

tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagtgaa caaaaacgtg 417

gactagcagc tttctttttt cctttgcaaa atcaatgatg gaggtaaaag tgtccattt 477

tgtcttcctc aataaagaac ttatcatcat aat 510

<210> 19

<211> 81

<212> PRT

<213> Conus textile

40

A

<400> 19
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu
 20 25 30
 Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly
 35 40 45
 Cys Met Ala Trp Phe Gly Leu Cys Ser Arg Asp Ser Glu Cys Cys Ser
 50 55 60
 Asn Ser Cys Asp Val Thr Arg Cys Glu Leu Met Pro Phe Pro Pro Asp
 65 70 75 80
 Trp

<210> 20
 <211> 441
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (16)..(243)

<400> 20
 ggaaaaactt ttatc atg gag aaa ctg aca atc ctg ctc ctt gtt gct gct 51
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala
 1 5 10
 gta ctg atg tcg acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc 99
 Val Leu Met Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser
 15 20 25
 cgg aag gcg gag atc aac ttt tct gaa aca aga aag ttg gcg aga aac 147
 Arg Lys Ala Glu Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn
 30 35 40
 aag cag aaa cgc tgc aaa act tat tca aag tat tgt gaa gct gac tcg 195
 Lys Gln Lys Arg Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser
 45 50 55 60
 gaa tgc tgt acc gaa cag tgt gta agg tct tac tgc acg ttg ttt gga 243
 Glu Cys Cys Thr Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
 65 70 75
 tgaattcgga ccacaagcca tccgatatca cccctctcct cttcagaggc ttcaaggctt 303
 ttgttatcct tttgaagaat ctttatcgag taaacataag tagacaagct ttttttttcc 363
 tttgcaaaat gaagaatgat ggcaaaaagc cccccatttt gtcttcatca ataaagaact 423
 cgctatcaga ataaaaaa 441

<210> 21
 <211> 76
 <212> PRT
 <213> Conus textile

[illegible]

42 A

Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu
 20 25 30
 Phe Ser Lys Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys
 35 40 45
 Ser Val Trp Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp
 50 55 60
 Cys His Glu Thr Cys Ile Phe Gly Trp Glu Val
 65 70 75

<210> 24
 <211> 533
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (110)..(337)

<400> 24
 ctctgccggt tgacacntca tctactctct cagtctccct gacagctgcc ttcagtcgac 60
 cctgccgtca tctcagcgca gacttgataa gaagtgaaaa acctttatc atg gag aaa 118
 Met Glu Lys
 1
 ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 166
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 5 10 15
 ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214
 Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe
 20 25 30 35
 tta tta aaa aga aag aga gct gct gac agg ggg atg tgg ggc gaa tgc 262
 Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys
 40 45 50
 aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310
 Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu
 55 60 65
 gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357
 Asp Cys Glu Gly Ser Cys Thr Met Trp
 70 75
 ccatctgaca tcaccactct cctcttcaga ggcttcaagg cttttgtttt ctttttgaat 417
 aatcttttacg agtaaacaaa taagtagact agcgcgtttt tttccctttg agaaatcaat 477
 gatggaggta aatagcttcc tattttgtct tattcaataa agaacttatc ataata 533

<210> 25
 <211> 76
 <212> PRT
 <213> Conus textile

<400> 25
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn
 20 25 30
 Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp
 35 40 45
 Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys
 50 55 60
 Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
 65 70 75

<210> 26
 <211> 408
 <212> DNA
 <213> Conus gloriamaris

<220>
 <221> CDS
 <222> (2)..(211)

<400> 26
 g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 49
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 1 5 10 15
 ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97
 Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe
 20 25 30
 ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145
 Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser
 35 40 45
 cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193
 Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser
 50 55 60

cgc tgc ata ttg gcg tta tgaactctga ccacaagcca tccgacatca 241
 Arg Cys Ile Leu Ala Leu
 65 70

ccactctcct cttcagaggc ttcaaggctt tttgtttttc ttttgaagaa tctttacgag 301
 tgaacaaata agtagaatag cacgtttttc cccctttgca aaatcaataa tggagggttaa 361
 aaaaaaactt ctgtcttctt caataaagaa gttatcataa taaaaaa 408

<210> 27
 <211> 70
 <212> PRT
 <213> Conus gloriamaris

<400> 27
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 1 5 10 15
 Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe

	20		25		30
Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser	35	40	45		
Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser	50	55	60		
Arg Cys Ile Leu Ala Leu	65	70			

<210> 28
 <211> 278
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (4)..(222)

<400> 28
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg 48
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu
 1 5 10 15
 tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat 96
 Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn
 20 25 30
 ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc 144
 Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys
 35 40 45
 gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg 192
 Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu
 50 55 60
 gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaagcca 242
 Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly
 65 70

tccgacatca ccactctcct cttcagagtc ttcaag 278

<210> 29
 <211> 73
 <212> PRT
 <213> Conus marmoreus

<400> 29
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe
 20 25 30
 Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu
 35 40 45
 Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp
 50 55 60
 Cys Glu Met Tyr Cys Thr Gln Ile Gly

65

70

<210> 30
<211> 287
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (4)..(231)

<400> 30
atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg ata 48
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile
1 5 10 15
ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96
Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala
20 25 30
gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144
Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val
35 40 45
cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192
Arg Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys
50 55 60
tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241
Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
65 70 75
ccacaagcca tccgatatca ccactctcct gttcagagtc ttcaag 287

<210> 31
<211> 76
<212> PRT
<213> Conus marmoreus

<400> 31
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile Pro
1 5 10 15
Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu
20 25 30
Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg
35 40 45
Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser
50 55 60
Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
65 70 75

<210> 32
<211> 278
<212> DNA
<213> Conus marmoreus

<220>

<221> CDS
<222> (4)..(213)

<400> 32
atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
1 5 10 15
acg acc cag gcc cta tat caa gaa aaa cgc cga aag gag atg atc aat 96
Thr Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn
20 25 30
ttt tta tca aaa gga aag ata aat gct gag agg cgg aac ggc gga tgc 144
Phe Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys
35 40 45
aaa gct act tgg atg tct tgt tca tgc ggc tgg gaa tgc tgt tct atg 192
Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met
50 55 60
agt tgt gac atg tac tgc gga tagataggat gaactctgac cacaagccat 243
Ser Cys Asp Met Tyr Cys Gly
65 70
ccgacatcac cactctcctc ttcagagtct tcaag 278

<210> 33
<211> 70
<212> PRT
<213> Conus marmoreus

<400> 33
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Thr
1 5 10 15
Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn Phe
20 25 30
Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys Lys
35 40 45
Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met Ser
50 55 60
Cys Asp Met Tyr Cys Gly
65 70

<210> 34
<211> 528
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (98)..(316)

<400> 34
gcacgtcatc ttctctctca gtctgcctga cagctgcctt cagtcacccc tgccgtcatc 60
tcagcgtaga cttggtaaga agtgaaaaac atttatac atg cag aaa ctg ata atc 115
Met Gln Lys Leu Ile Ile
1 5

ctg ctt ctt gtt gct gct gtg ctg atg tgc acc cag gcc gtg ctt caa 163
Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala Val Leu Gln
10 15 20

gaa aaa cgc cca aag gag aag atc aag ctt tta tca aag aga aag aca 211
Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu Leu Ser Lys Arg Lys Thr
25 30 35

gat gct gag aag cag cag aag cgc ctt tgc ccg gat tac acg gag cct 259
Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys Pro Asp Tyr Thr Glu Pro
40 45 50

tgt tca cat gcc cat gaa tgc tgt tca tgg aat tgt tat aat ggg cac 307
Cys Ser His Ala His Glu Cys Cys Ser Trp Asn Cys Tyr Asn Gly His
55 60 65 70

tgt acg gga tgaactcgga ccacaagcca tccgacatca ccactctcct 356
Cys Thr Gly

cttcagagggc ttcaagactt ttgtttctgat tttggacaat ctttacgagt aaacaaataa 416

ttagactagc acttttttttc ccctttgcaa aatcaatgat ggaggtaaaa agcctcccat 476

tttgtcttca tcaataaaga acttatcatc aaaaaaaaaa aaaaaaaaaa aa 528

<210> 35

<211> 73

<212> PRT

<213> Conus textile

<400> 35

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu
20 25 30

Leu Ser Lys Arg Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys
35 40 45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp
50 55 60

Asn Cys Tyr Asn Gly His Cys Thr Gly
65 70

<210> 36

<211> 26

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 18 is Trp or 6-bromo-Trp; Xaa at
residues 7 and 14 are Glu or
gamma-carboxyglutamate; Xaa at residues 3 and 8
are Pro or hydroxy-Pro.

<400> 36

Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys
1 5 10 15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr
20 25

<210> 37
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
gamma-conopeptide sequence for probe

<220>
<221> PEPTIDE
<222> (1)
<223> Xaa is Glu or Gln.

<400> 37
Xaa Cys Cys Ser
1

<210> 38
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
probe for consensus gamma-conopeptide sequence.

<400> 38
sartgytggya gy

12

<210> 39
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
probe for consensus gamma-conopeptide sequence.

<400> 39
sartgytgyt cn

12

<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
pro-gamma-conopeptide sequence for probe.

<400> 40
Ile Leu Leu Val Ala Ala Val Leu
1 5

<210> 41

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 probe for consensus pro-gamma-conopeptide
 sequence.

<400> 41
 athytntyng tngcngcngt nytn

24

<210> 42
 <211> 32
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 14 and 26 are
 gamma-carboxyglutamate; Xaa at residue 31 is
 hdroxy-Pro.

<400> 42
 Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
 1 5 10 15
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
 20 25 30

<210> 43
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 9 and 13 are
 gamma-carboxyglutamate.

<400> 43
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser
 1 5 10 15
 Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe
 20 25

<210> 44
 <211> 8
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> MOD_RES
 <222> (2)
 <223> Xaa at residue 2 is carboxymethylCys

<400> 44
Asp Xaa Thr Ser Trp Phe Gly Arg
1 5

<210> 45
<211> 24
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residues 6 and 18 are
gamma-carboxyglutamate; Xaa at residue 23 is
hydroxy-Pro.

<400> 45
Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr
1 5 10 15

Xaa Xaa Leu Tyr Ala Phe Xaa Ser
20

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for M13
universal priming site.

<400> 46
tttcccagtc acgacgtt

18

<210> 47
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for M13
reverse priming site.

<400> 47
cacacaggaa acagctatg

19